K

EXHIBIT 2

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                        DIALIGN 2.1
                        * * * * * * * * * *

            Developed by Burkhard Morgenstern, Said Abdeddai
m, Kornelie Frech,
            Klaus Hahn, Thomas Werner, Jens Stoye, Andreas D
ress

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        Published research assisted by DIALIGN 2 should
cite:

        B. Morgenstern (1999),
        "DIALIGN 2: improvement of the segment-to-segm
ent

        approach to multiple sequence alignment."
        Bioinformatics 15, 203 - 210.



    Options:
    ========

    1) proteine sequences aligned
    2) 5 "*" characters for regions of maximum similarity


    Aligned sequences:          length:
    =================           =======

    1)      855444              501
    2)          2               501

    Average sequence length: 501.000



 Please note that only upper-case letters are considered to
be aligned.
 For more information, have a look at the user guide

    http://bibiserv.techfak.uni-bielefeld.de/dialign/user_gu
```

ide2.html

Alignment (DIALIGN format):
==============================

855444   1   MAQALPWLLL WMGAGVLPAH GTQHGIRLPL RSGLGGAPL
G LRLPRETDEE
2   1   MAQALPWLLL WMGAGVLPAH GTQHGIRLPL RSGLGGAPL
G LRLPRETDEE

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855444   51   PEEPGRRGSF VEMVDNLRGK SGQGYYVEMT VGSPPQTLN
I LVDTGSSNFA
2   51   PEEPGRRGSF VEMVDNLRGK SGQGYYVEMT VGSPPQTLN
I LVDTGSSNFA

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855444          101    VGAAPHPFLH RYYQRQLSST YRDLRKGVYE PYTQGKWEG
E LGTDLVSIPH
2               101    VGAAPHPFLH RYYQRQLSST YRDLRKGVYV PYTQGKWEG
E LGTDLVSIPH


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855444          151    GPNVTVRANI AAITESDKFF INGSNWEGIL GLAYAEIAR
P DDSLEPFFDS
2               151    GPNVTVRANI AAITESDKFF INGSNWEGIL GLAYAEIAR
P DDSLEPFFDS


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*  *********          ********* ********* ********* *********


855444          201    LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGG
I DHSLYTGSLW
2               201    LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGG
I DHSLYTGSLW


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*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *
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```
855444        251     YTPIRREWYY  EVIIVRVEIN  GQDLKMDCKE  YNYDKSIVD
S GTTNLRLPKK
2             251     YTPIRREWYY  EVIIVRVEIN  GQDLKMDCKE  YNYDKSIVD
S GTTNLRLPKK
```

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*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *

*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *

*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * * *  * * * * * * * *

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855444        301     VFEAAVKSIK  AASSTEKFPD  GFWLGEQLVC  WQAGTTPWN
I FPVISLYLMG
2             301     VFEAAVKSIK  AASSTEKFPD  GFWLGEQLVC  WQAGTTPWN
I FPVISLYLMG
```

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*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *

*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *

*  * * * * * * * * *          * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *

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855444        351     EVTNQSFRIT  ILPQQYLRPV  EDVATSQDDC  YKFAISQSS
T GTVMGAVIME
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```
2                 351    EVTNQSFRIT ILPQQYLRPV EDVATSQDDC YKFAISQSS
T GTVMGAVIME
```

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*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

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855444            401    GFYVVFDRAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLD
M EDCGYNIPQT
2                 401    GFYVVFDRAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLD
M EDCGYNIPQT
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*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

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```
855444            451    DESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQ
H DDFADDISLL
2                 451    DESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQ
H DDFADDISLL
```

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*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

*  * * * * * * * *          * * * * * * * * *  * * * * * * * * *  * * * * * * * * *  * * * * * * * *

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EXHIBIT 2

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855444                           K
2                                K

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Alignment (FASTA format):
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>855444
MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHPFLHRYYQRQLSSTYRDLRKGVYEPYTQGKWEGELGTDLVSIPH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK
VFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMG
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL
K

>2
MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK
VFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMG
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL

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